

- 45 -

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: (Other than US) AMRAD OPERATIONS PTY LTD  
(US only) Suzanne Cory, Jerry McKee Adams, Leonie Gibson and  
Sean P Holmgreen

- (ii) TITLE OF INVENTION: ~~THERAPEUTIC MOLECULES~~  
*A Novel Mammalian Gene, bcl-2, belongs to the bcl-2*  
*family of Apoptosis-controlling*  
*genes.*
- (iii) NUMBER OF SEQUENCES: 9

(iv) ~~CORRESPONDENCE ADDRESS:~~

- (A) ADDRESSEE: DAVIES COLLISON CAVE  
(B) STREET: 1 LITTLE COLLINS STREET  
(C) CITY: MELBOURNE  
(D) STATE: VICTORIA  
(E) COUNTRY: AUSTRALIA  
(F) ZIP: 3000

(v) ~~COMPUTER READABLE FORM:~~

- (A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) ~~SOFTWARE: PatentIn Release #1.0, Version #1.25~~

*Prior*  
(vi) ~~CURRENT~~ APPLICATION DATA:

- (A) APPLICATION NUMBER: ~~PCT-INTERNATIONAL~~ 09/155,327  
(B) FILING DATE: 27-MAR-1997

(vi) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: PN 8965  
(B) FILING DATE: 27-MAR-1996

(viii) ~~ATTORNEY/AGENT INFORMATION:~~

- (A) NAME: HUGHES DR, E JOHN L  
(C) REFERENCE/DOCKET NUMBER: EJH/EK

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: +61 3 9254 2777  
(B) ~~TELEFAX: +61 3 9254 2770~~

- 46 -

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCTCTAGAAC TGGGG~~(A/C)~~G~~(A/G)~~T~~(G/T)~~GCCTT ~~(C/T)~~TT

33

$\begin{matrix} n & h & n & r & n & n & y \end{matrix}$

wherein n is inosine at position 16, 19, 22 and 25.

## (2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 9 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Xaa

Asn Trp Gly Arg ~~(Ile/Val)~~ Val Ala Phe Phe

5

wherein Xaa is Ile or Val.

## (2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 31 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGAATTCCTA GCC~~(C/T)~~~~(G/T)~~TCTTGATCC A

31

$\begin{matrix} n & n & k & n \end{matrix}$

wherein n is inosine at position 14, 17 and 20.

- 47 -

## (2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Trp Ile Gln (~~Asp/Glu~~) (~~Asn/Gln~~) Gly Gly Trp

Xaa 5 Xaa

wherein Xaa at position 4 is Asp or Glu, <sup>and</sup> Xaa at position 5 is Asn or Gln.

## (2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 14 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Ala Thr Pro Ala Ser Thr Pro Asp Thr Arg Ala Leu Val

5

10

## (2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 583 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

- 48 -

ATG GCG ACC CCA GCC TCG GCC CCA GAC ACA CGG GCT CTG GTG GCA GAC	48
Met Ala Thr Pro Ala Ser Ala Pro Asp Thr Arg Ala Leu Val Ala Asp	
1 5 10 15	
TTT GTA GGT TAT AAG CTG AGG CAG AAG GGT TAT GTC TGT GGA GCT GGC	96
Phe Val Gly Tyr Lys Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly	
20 25 30	
CCC GGG GAG GGC CCA GCA GCT GAC CCG CTG CAC CAA GCC ATG CGG GCA	144
Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala	
35 40 45	
GCT GGA GAT GAG TTC GAG ACC CGC TTC CGG CGC ACC TTC TCT GAT CTG	192
Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu	
50 55 60	
GCG GCT CAG CTG CAT GTG ACC CCA GGC TCA GCC CAG CAA CGC TTC ACC	240
Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr	
65 70 75 80	
CAG GTC TCC GAC GAA CTT TTT CAA GGG GGC CCC AAC TGG GGC CGC CTT	288
Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu	
85 90 95	
GTA GCC TTC TTT <del>CTC</del> TTT GGG GCT GCA CTG TGT GCT GAG AGT GTC AAC	336
Val Ala Phe Phe <del>Leu</del> Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn	
100 Val 105 110	
AAG GAG ATG GAA CCA CTG GTG GGA CAA GTG CAG GAG TGG ATG GTG GCC	384
Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Glu Trp Met Val Ala	
115 120 125	
TAC CTG GAG ACG CGG CTG <del>GTC</del> GAC TGG ATC CAC AGC AGT GGG GGC TGG	432
Tyr Leu Glu Thr Arg Leu <del>Val</del> Asp Trp Ile His Ser Ser Gly Gly Trp	
130 135 140	
GCG GAG TTC ACA GCT CTA TAC GGG GAC GGG GCC CTG GAG GAG GCG CGG	480
Ala Glu Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Glu Ala Arg	
145 150 155 160	
CGT CTG CGG GAG GGG AAC TGG GCA TCA GTG AGG ACA GTG CTG ACG GGG	528
Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Arg Thr Val Leu Thr Gly	
165 170 175	
GCC GTG GCA CTG GGG GCC CTG GTA ACT GTA GGG GCC TTT TTT GCT AGC	576
Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser	
180 185 190	
AAG TGA A	583
Lys *	

- 49 -

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19<sup>3</sup> amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ala Thr Pro Ala Ser Ala Pro Asp Thr Arg Ala Leu Val Ala Asp  
 1 5 10 15

Phe Val Gly Tyr Lys Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly  
 20 25 30

Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala  
 35 40 45

Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu  
 50 55 60

Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr  
 65 70 75 80

Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu  
 85 90 95

Val Ala Phe Phe <sup>Val</sup> ~~Leu~~ Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn  
 100 105 110

Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Glu Trp Met Val Ala  
 115 120 125

Tyr Leu Glu Thr Arg Leu <sup>Ala</sup> ~~Val~~ Asp Trp Ile His Ser Ser Gly Gly Trp  
 130 135 140

Ala Glu Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Glu Ala Arg  
 145 150 155 160

Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Arg Thr Val Leu Thr Gly  
 165 170 175

Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser  
 180 185 190

Lys \*

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 582 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single

- 50 -

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATG	<sup>G</sup> CG	ACC	CCA	GCC	TCA	ACC	CCA	GAC	ACA	<sup>G</sup> CG	GCT	CTA	GTG	GCT	GAC	48
Met	<del>Pro</del>	Thr	Pro	Ala	Ser	Thr	Pro	Asp	Thr	Arg	Ala	Leu	Val	Ala	Asp	
1	Ala			5					10				15			
TTT	GTA	GGC	TAT	AGG	CTG	AGG	CAG	AAG	GGT	TAT	GTC	TGT	GGA	GCT	<sup>C</sup> GG	96
Phe	Val	Gly	Tyr	Arg	Leu	Arg	Gln	Lys	Gly	Tyr	Val	Cys	Gly	Ala	Gly	
		20					25					30				
CCT	GGG	GAA	GGC	CCA	GCC	GCC	GAC	CCG	CTG	CAC	CAA	GCC	ATG	CGG	GCT	144
Pro	Gly	Glu	Gly	Pro	Ala	Ala	Asp	Pro	Leu	His	Gln	Ala	Met	Arg	Ala	
		35					40					45				
GCT	GGA	GAC	GAG	TTT	GAG	ACC	CGT	TTC	CGC	CGC	ACC	TTC	TCT	GAC	CTG	192
Ala	Gly	Asp	Glu	Phe	Glu	Thr	Arg	Phe	Arg	Arg	Thr	Phe	Ser	Asp	Leu	
		50					55				60					
GCC	GCT	CAG	CTA	CAC	GTG	ACC	CCA	GGC	TCA	GCC	CAG	CAA	CGC	TTC	ACC	240
Ala	Ala	Gln	Leu	His	Val	Thr	Pro	Gly	Ser	Ala	Gln	Gln	Arg	Phe	Thr	
		65			70				75					80		
CAG	GTT	TCC	GAC	GAA	CTT	TTC	CAA	GGG	GGC	CCT	AAC	TGG	GGC	CGT	CTT	288
Gln	Val	Ser	Asp	Glu	Leu	Phe	Gln	Gly	Gly	Pro	Asn	Trp	Gly	Arg	Leu	
			85						90					95		
GTG	GCA	TTC	TTT	GTC	TTT	GGG	GCT	GCC	CTG	TGT	GCT	GAG	AGT	GTC	AAC	336
Val	Ala	Phe	Phe	Val	Phe	Gly	Ala	Ala	Leu	Cys	Ala	Glu	Ser	Val	Asn	
			100						105					110		
AAA	GAA	ATG	GAG	CCT	TTG	GTG	GGA	CAA	<sup>G</sup> GT	CAG	GAT	TGG	<sup>G</sup> AT	GTG	GCC	384
Lys	Glu	Met	Glu	Pro	Leu	Val	Gly	Gln	Val	Gln	Asp	Trp	<del>Ile</del>	Val	Ala	
		115						120				125	Met			
TAC	CTG	GAG	ACA	CGT	CTG	GCT	GAC	TGG	ATC	CAC	AGC	AGT	GGC	GGC	TGG	432
Tyr	Leu	Glu	Thr	Arg	Leu	Ala	Asp	Trp	Ile	His	Ser	Ser	Gly	Gly	Trp	
		130					135				140					
GCG	<sup>G</sup> GA	TTC	ACA	GCT	CTA	TAC	GGG	GAC	GGG	GCC	CTG	GAG	<sup>G</sup> GA	GCA	CGG	480
Ala	<del>Asp</del>	Phe	Thr	Ala	Leu	Tyr	Gly	Asp	Gly	Ala	Leu	Glu	<del>Asp</del>	Ala	Arg	
145	Glu				150				155			Glu		160		
CGT	CTG	CGG	GAG	<sup>G</sup> GG	AAC	TGG	GCA	<sup>C</sup> TGA	GTG	<sup>G</sup> AG	ACA	GTG	<sup>C</sup> GTG	ACG	GGG	528
Arg	Leu	Arg	Glu	Gly	Asn	Trp	Ala	<del>Ser</del>	Val	<del>Ser</del>	Thr	Val	<del>Val</del>	Thr	Gly	
			165					170				Leu		175		
GCC	GTG	GCA	CTG	GGG	GCC	CTG	GTA	ACT	GTA	GGG	GCC	TTT	TTT	GCT	AGC	576

- 51 -

Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser  
 180 185 190

AAG TGA  
 Lys

582

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met <sup>Ala</sup>~~Pro~~ Thr Pro Ala Ser Thr Pro Asp Thr Arg Ala Leu Val Ala Asp  
 1 5 10 15

Phe Val Gly Tyr Arg Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly  
 20 25 30

Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala  
 35 40 45

Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu  
 50 55 60

Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr  
 65 70 75 80

Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu  
 85 90 95

Val Ala Phe Phe Val Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn  
 100 105 110

Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Asp Trp <sup>Met</sup>~~Ile~~ Val Ala  
 115 120 125

Tyr Leu Glu Thr Arg Leu Ala Asp Trp Ile His Ser Ser Gly Gly Trp  
 130 135 140

Ala <sup>Glu</sup>~~Asp~~ Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu <sup>Glu</sup>~~Asp~~ Ala Arg  
 145 150 155 160

Arg Leu Arg Glu Gly Asn Trp Ala <sup>Ser</sup>~~Val~~ Val <sup>Arg</sup>~~Ser~~ Thr Val <sup>Leu</sup>~~Val~~ Thr Gly  
 165 170 175

Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser  
 180 185 190

Lys